1642

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:                    ENTERED
 4
 5     (i)   APPLICANT: Adair, John R.
 6                      Athwal, Diljeet S.
 7                      Emtage, John S.
 8
 9    (ii)      TITLE OF INVENTION: Humanised Antibodies
10
11    (iii)     NUMBER OF  SEQUENCES: 30
12
13    (iv)      CORRESPONDENCE  ADDRESS:
14         (A)  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
15         (B)  STREET: One Liberty Place - 46th Floor
16         (C)  CITY:   Philadelphia
17         (D)  STATE: PA
18         (E)  COUNTRY: USA
19         (F)  ZIP: 19103
20
21    (v)   COMPUTER  READABLE  FORM:
22         (A)  MEDIUM TYPE: Floppy disk
23         (B)  COMPUTER: IBM PC compatible
24         (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
25         (D)  SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27    (vi)      CURRENT APPLICATION DATA:
28         (A)  APPLICATION NUMBER: US 08/846,658
29         (B)  FILING DATE: 01-MAY-1997
30         (C)  CLASSIFICATION:
31
32    (viii)    ATTORNEY/AGENT INFORMATION:
33         (A)  NAME: Trujillo, Doreen Yatko
34         (B)  REGISTRATION NUMBER: 35,719
35         (C)  REFERENCE/DOCKET NUMBER: CARP-0057
36
37    (ix)      TELECOMMUNICATION INFORMATION:
38         (A)  TELEPHONE: (215) 568-3100
39         (B)  TELEFAX: (215) 568-3439
40
41
42    (2) INFORMATION FOR SEQ ID NO:1:
43
44     (i) SEQUENCE CHARACTERISTICS:
45         (A) LENGTH: 20 base pairs
46         (B) TYPE: nucleic  acid
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47          (C) STRANDEDNESS: single
48          (D) TOPOLOGY: linear
49
50      (ii) MOLECULE TYPE: cDNA
51
52
53      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55  TCCAGATGTT AACTGCTCAC                                           20
56
57  (2) INFORMATION FOR SEQ ID NO:2:
58
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 23 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS:  single
63          (D) TOPOLOGY:  linear
64
65      (ii) MOLECULE TYPE: cDNA
66
67
68
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70
71  CAGGGGCCAG TGGATGGATA GAC                                       23
72
73  (2) INFORMATION FOR SEQ ID NO:3:
74
75      (i) SEQUENCE CHARACTERISTICS:
76          (A) LENGTH: 9 amino acids
77          (B) TYPE: amino  acid
78          (C) STRANDEDNESS:  single
79          (D) TOPOLOGY:  linear
80
81      (ii) MOLECULE TYPE: peptide
82
83
84
85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
86
87  Leu Glu Ile Asn Arg Thr Val Ala Ala
88  1               5
89
90  (2) INFORMATION FOR SEQ ID NO:4:
91
92      (i) SEQUENCE CHARACTERISTICS:
93          (A) LENGTH: 943 base pairs
94          (B) TYPE: nucleic acid
95          (C) STRANDEDNESS:  single
96          (D) TOPOLOGY:  linear
97
98      (ii) MOLECULE TYPE: cDNA
99
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100
101          (ix) FEATURE:
102              (A) NAME/KEY: CDS
103              (B) LOCATION: 18..722
104
105          (ix) FEATURE:
106              (A) NAME/KEY: mat_peptide
107              (B) LOCATION: 84..722
108
109
110          (xi) SEQUENCE DESCRIPTION: SEQ  ID  NO:4:
111
112   GAATTCCCAA AGACAAA ATG GAT TTT CAA GTG CAG ATT TTC AGC TTC CTG              50
113                       Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu
114                       -22     -20                     -15

115
116   CTA ATC AGT GCC TCA GTC ATA ATA TCC AGA GGA CAA ATT GTT CTC ACC           98
117   Leu Ile Ser Ala Ser Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr
118   -10              -5                     1               5
119
120   CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATG          146
121   Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
122              10              15                  20
123
124   ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG TAC CAG CAG          194
125   Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
126              25              30                  35
127
128   AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA TCC AAA CTG          242
129   Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
130          40                  45                  50
131
132   GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT GGG ACC TCT          290
133   Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser
134          55              60                  65
135
136   TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT GCC ACT TAT          338
137   Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr
138   70                  75              80                  85
139
140   TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC TCG GGG ACA          386
141   Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr
142              90                  95                  100
143
144   AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GTA TCC ATC TTC          434
145   Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe
146              105                 110                 115
147
148   CCA CCA TCC AGT GAG CAG TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC          482
149   Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
150          120                 125                 130
151
152   TTC TTG AAC AAC TTC TAC CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT          530
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153   Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
154       135             140             145
155
156
157   GAT GGC AGT GAA CGA CAA AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG      578
158   Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
159   150             155             160             165
160
161   GAC AGC AAA GAC AGC ACC TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC      626
162   Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
163             170             175             180
164
165   AAG GAC GAG TAT GAA CGA CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC      674
166   Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
167             185             190             195
168
169   AAG ACA TCA ACT TCA CCC ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT      722
170   Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
171             200             205             210
172
173   TAGAGACAAA GGTCCTGAGA CGCCACCACC AGCTCCCAGC TCCATCCTAT CTTCCCTTCT     782
174
175   AAGGTCTTGG AGGCTTCCCC ACAAGCGCTT ACCACTGTTG CGGTGCTCTA AACCTCCTCC     842
176
177   CACCTCCTTC TCCTCCTCCT CCCTTTCCTT GGCTTTTATC ATGCTAATAT TTGCAGAAAA     902
178
179   TATTCAATAA AGTGAGTCTT TGCCTTGAAA AAAAAAAAAA A                          943
180
181
182   (2) INFORMATION FOR SEQ ID NO:5:
183
184          (i) SEQUENCE CHARACTERISTICS:
185                (A) LENGTH: 235 amino acids
186                (B) TYPE: amino acid
187                (D) TOPOLOGY: linear
188
189         (ii) MOLECULE TYPE: protein
190
191         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
192
193   Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
194   -22      -20             -15             -10
195
196   Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
197       -5              1               5                   10
198
199   Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
200             15              20                  25
201
202   Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
203             30              35                  40
204
205   Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
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206                45                        50                        55
207
208   Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
209        60                  65                  70
210
211   Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
212    75                  80                  85                  90
213
214
215   Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
216                  95                  100                 105
217
218   Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
219            110                 115                 120
220
221   Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
222            125                 130                 135
223
224   Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
225        140                 145                 150
226
227   Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
228   155                 160                 165                 170
229
230   Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
231                  175                 180                 185
232
233   Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
234            190                 195                 200
235
236   Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
237        205                 210
238
239   (2) INFORMATION FOR SEQ ID NO:6:
240
241       (i) SEQUENCE CHARACTERISTICS:
242           (A) LENGTH: 1570 base pairs
243           (B) TYPE: nucleic  acid
244           (C) STRANDEDNESS: single
245           (D) TOPOLOGY: linear
246
247   (ii) MOLECULE TYPE:   cDNA
248
249
250   (ix) FEATURE:
251       (A) NAME/KEY:   CDS
252       (B) LOCATION:   41..1444
253
254   (ix) FEATURE:
255           (A) NAME/KEY:   mat_peptide
256           (B) LOCATION:   98..1444
257
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/846,658A*

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Line   Error   Original Text